

AMENDMENTS TO THE CLAIMS

1. (currently amended) A method of determining at least one unknown ~~of the~~ biochemical ~~and or~~ biophysical ~~properties~~ property of a target protein, said method comprising:
 - a) ~~providing~~ analyzing a database comprising ~~protein~~ (i) sequence information for a plurality of proteins and (ii) at least one of: ~~protein~~ biochemical properties and ~~protein~~ biophysical properties for the plurality of proteins,
 - b) ~~analyzing the database~~ using a data-mining technique to ~~correlate~~ produce correlations between (i) the protein sequence information for a given protein and (ii) at least one of: one or more of the following: protein sequence, biochemical properties[[,]] and biophysical properties of the given protein, and
 - e) ~~analyzing b)~~ applying the correlations from the plurality of proteins to the sequence of the target protein using the correlations to determine it's thereby determining the unknown biochemical or biophysical properties property of the target protein.
2. (original) The method of claim 1, wherein the property being determined is a biophysical property.
3. (previously presented) The method of claim 2, wherein the biophysical property is thermal stability, solubility, isoelectric point, pH stability, crystalizability, conditions of crystallization, aggregation state, heat capacity (DC_p), resistance to chemical denaturation, resistance to proteolytic degradation, amide hydrogen exchange data, behavior on chromatographic matrices, electrophoretic mobility, and resistance to degradation during mass spectrometry.
4. (withdrawn) The method of claim 3, wherein the biophysical property is thermal stability.
5. (original) The method of claim 3, wherein the biophysical property is solubility.
6. (withdrawn) The method of claim 3, wherein the biophysical property is crystalizability.
7. (withdrawn) The method of claim 3, wherein the biophysical property is conditions of crystallization.
8. (withdrawn) The method of claim 3, wherein the biophysical property is isoelectric point.

9. (withdrawn) The method of claim 3, wherein the biophysical property is pH stability.
10. (withdrawn) The method of claim 3, wherein the biophysical property is aggregation state.
11. (withdrawn) The method of claim 3, wherein the biophysical property is heat capacity (DC_p).
12. (withdrawn) The method of claim 3, wherein the biophysical property is resistance to chemical denaturation.
13. (withdrawn) The method of claim 3, wherein the biophysical property is resistance to proteolytic degradation.
14. (withdrawn) The method of claim 3, wherein the biophysical property is amide hydrogen exchange data.
15. (withdrawn) The method of claim 3, wherein the biophysical property is behavior on chromatographic matrices.
16. (withdrawn) The method of claim 3, wherein the biophysical property is electrophoretic mobility.
17. (withdrawn) The method of claim 3, wherein the biophysical property is resistance to degradation during mass spectrometry.
18. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from nuclear magnetic resonance.
19. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from X-ray crystallography.
20. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from circular dichroism.
21. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from light scattering.
22. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from atomic adsorption.

23. (withdrawn) The method of claim 3, wherein biophysical property is the results obtained from fluorescence.
24. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from fluorescence quenching.
25. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from mass spectroscopy.
26. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from infrared spectroscopy.
27. (withdrawn) The method of claim 3, wherein biophysical property is the results obtained from electron microscopy.
28. (withdrawn) The method of claim 3, wherein the biophysical property is the results obtained from atomic force microscopy.
29. (withdrawn) The method of claim 1, wherein the property being determined is a biochemical property.
30. (withdrawn) The method of claim 29, wherein the biochemical property is expressability, protein yield, small-molecule binding, subcellular localization, utility as a drug target, protein-protein interactions or protein-ligand interactions.
31. (withdrawn) The method of claim 30, wherein the biochemical property is small-molecule binding.
32. (withdrawn) The method of claim 30, wherein the biochemical property is protein yield.
33. (withdrawn) The method of claim 30, wherein the biochemical property is expressability.
34. (withdrawn) The method of claim 30, wherein the biochemical property is subcellular localization.
35. (withdrawn) The method of claim 30, wherein the biochemical property is utility as a drug target.
36. (withdrawn) The method of claim 30, wherein the biochemical property is protein-protein interactions.

37. (withdrawn) The method of claim 30, wherein the biochemical property is protein-ligand interactions.
38. (original) The method of claim 1, wherein the data-mining technique is selected from the group decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and support vector machines.
39. (original) The method of claim 38, wherein the data-mining technique is decision-tree analysis.
40. (original) The method of claim 38, wherein the data-mining technique is case-based reasoning.
41. (original) The method of claim 38, wherein the data-mining technique is Bayesian classifier.
42. (original) The method of claim 38, wherein the data-mining technique is simple linear discriminant analysis.
43. (original) The method of claim 38, wherein the data-mining technique is support vector machines.
44. (withdrawn) A method of optimizing high-throughput protein structure determination, said method comprising the steps of :
 - a) providing a database comprising protein sequence information and protein biochemical and biophysical properties,
 - b) analyzing the database using a data-mining technique,
 - c) determining correlations between protein sequence and biochemical or biophysical properties,
 - d) analyzing the sequence of a protein using said correlations to determine its biochemical or biophysical properties, and
 - e) optimizing the throughput of the protein structure determination based on said biochemical or biophysical properties by modifying the experimental procedures and/or modifying the protein sequence.
45. (withdrawn) The method of claim 44, wherein the data-mining technique is selected from the group decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and

46. (withdrawn) The method of claim 45, wherein the data-mining technique is decision-tree analysis.
47. (withdrawn) The method of claim 45, wherein the data-mining technique is case-based reasoning.
48. (withdrawn) The method of claim 45, wherein the data-mining technique is Bayesian classifier.
49. (withdrawn) The method of claim 45, wherein the data-mining technique is simple linear discriminant analysis.
50. (withdrawn) The method of claim 45, wherein the data-mining technique is support vector machines.
51. (withdrawn) A method of optimizing high-throughput protein purification, said method comprising the steps of :
 - a) providing a database comprising protein sequence information and protein biochemical and biophysical properties,
 - b) analyzing the database using a data-mining technique,
 - c) determining correlations between protein sequence and biochemical or biophysical properties,
 - d) analyzing the sequence of a protein using the correlations to determine its biochemical or biophysical properties, and
 - e) optimizing the throughput of the protein purification based on said biochemical or biophysical properties by modifying the experimental procedures and/or modifying the protein sequence.
52. (withdrawn) The method of claim 51, wherein the data-mining technique is selected from the group decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and support vector machines.
53. (withdrawn) The method of claim 52, wherein the data-mining technique is decision-tree analysis.
54. (withdrawn) The method of claim 52, wherein the data-mining technique is case-based reasoning.

55. (withdrawn) The method of claim 52, wherein the data-mining technique is Bayesian classifier.
56. (withdrawn) The method of claim 52, wherein the data-mining technique is simple linear discriminant analysis.
57. (withdrawn) The method of claim 52, wherein the data-mining technique is support vector machines.
58. (withdrawn) A method of optimizing high-throughput protein expression, said method comprising:
 - a) providing a database comprising protein sequence information and at least one of: protein biochemical properties and protein biophysical properties,
 - b) analyzing the database using a data-mining technique to correlate one or more of the following: protein sequence, biochemical properties, and biophysical properties,
 - c) analyzing the sequence of the protein using the correlations to determine at least one of the biochemical and the biophysical properties of the protein, and
 - d) optimizing throughput of the protein expression based on said biochemical or biophysical properties by modifying at least one of: experimental procedures and the protein sequence.
59. (withdrawn) The method of claim 58, wherein the data-mining technique is selected from the group decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and
60. (withdrawn) The method of claim 59, wherein the data-mining technique is decision-tree analysis.
61. (withdrawn) The method of claim 59, wherein the data-mining technique is case-based reasoning.
62. (withdrawn) The method of claim 59, wherein the data-mining technique is Bayesian classifier.
63. (withdrawn) The method of claim 59, wherein the data-mining technique is simple linear discriminant analysis.
64. (withdrawn) The method of claim 59, wherein the data-mining technique is support vector machines.

65. (withdrawn) A method of optimizing drug-target discovery, said method comprising the steps of :
- a) providing a database comprising protein sequence information and protein biochemical and biophysical properties,
 - b) analyzing the database using a data-mining technique,
 - c) determining correlations between protein sequence and biochemical or biophysical properties,
 - d) analyzing the sequence of a protein using the correlations to determine its biochemical or biophysical properties, and
 - e) optimizing drug-target discovery base on said biochemical or biophysical properties by modifying the experimental procedures and/or modifying the protein sequence.
66. (withdrawn) A method of screening proteins for drug-target discovery, said method comprising the steps of :
- a) providing a database comprising protein sequence information and protein biochemical and biophysical properties,
 - b) analyzing the database using a data-mining technique,
 - c) determining correlations between protein sequence and biochemical or biophysical properties,
 - d) analyzing the sequence of the protein using the correlations to determine its biochemical or biophysical properties, and
 - e) selecting proteins for analysis as a drug target based on their predicted biochemical and/or biophysical properties.
67. (currently amended) The method of claim [[2]] 1, wherein the database comprises sequence information for a plurality of proteins and biophyscial properties for the plurality of proteins, and wherein where the biophysical property is properties are based on data obtained from one or more of the following: nuclear magnetic resonance, X-ray crystallography, circular dichroism, light scattering, atomic adsorption, fluorescence, fluorescence quenching, mass spectroscopy, infrared spectroscopy, electron microscopy, and atomic force microscopy.
68. (currently amended) The method of claim 1, wherein the database comprises ~~protein~~ sequence information for a plurality of proteins and at least one of: ~~protein~~ biochemical

properties and ~~protein~~ biophysical properties for ~~a large number~~ the plurality of proteins, and wherein said biochemical properties and biophyscial properties ~~which~~ have been examined under uniform conditions.

69. (currently amended) The method of claim 1, wherein the database comprises ~~protein~~ sequence information for a plurality of proteins and at least one of: ~~protein~~ biochemical properties and ~~protein~~ biophysical properties for ~~a variety~~ the plurality of proteins, and wherein each ~~protein's~~ the biochemical properties and biophysical properties for a given protein have been determined under a variety of experimental conditions.
70. (withdrawn) The method of claim 58, wherein the database comprises protein sequence information and at least one of: protein biochemical properties and protein biophysical properties for a large number of proteins which have been examined under uniform conditions.
71. (withdrawn) The method of claim 58, wherein the database comprises protein sequence information and at least one of: protein biochemical properties and protein biophysical properties for a variety of proteins wherein each protein's biochemical properties and biophysical properties have been determined under a variety of experimental conditions.